Chapter 7
Breeding for Salinity Tolerance

Nand Kumar Fageria, Luís Fernando Stone and Alberto Baêta dos Santos

Abstract Soil salinity is a major factor adversely affecting crop yields worldwide. It is estimated that worldwide about 1 billion ha of land is affected by salinity. In addition, salinity problem is increasing at a rate of about 10% annually worldwide. Salinity can cause a combination of complex interactions that affect plant metabolism, susceptibility to injury or internal nutrient requirement. The negative interactions of salts with crop plants may reduce growth and consequently nutrient use efficiency. Management practices which can be adopted to reduce negative effects of salts on plant growth includes leaching salts from soil profile, use of amendments such as gypsum, and use of farmyard manners. However, use of salt-tolerant crop species or genotypes within species is a very attractive strategy to reduce cost of salt reclamation and environmental pollution. Although salt tolerance is relatively low in most crop species, it is encouraging that genetic variability exists not only among species but also among genotypes of same species. Salt-tolerant crop species are barley, cotton, oats, rye, triticale, sugar beet, guar, and canola or rapseed. Plant resistance responses include both salt avoidance (selective uptake or exclusion mechanisms and salt secretion, such as through salt glands) and salt tolerance (osmotic adjustment to maintain turgor pressure, tissue tolerance to specific toxic ions, e.g., Na and Cl, and tissue dehydration tolerance).

Keywords Absorption of nutrients · Genetic variability · Electrical conductivity · Salinity threshold · Dry matter or grain yield efficiency index · Breeding methods for salinity · Genetic markers · Quantitative trait loci (QLT) · Transgenic method

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7.1 Introduction

Soil salinity is a major factor which reduces crop production worldwide. Major areas affected by salts are located in North, central, and South Asia (Table 7.1). In South America, areas affected by salinity are about 85 million hectares, including saline and sodic soils. In Brazil, major soils affected by salinity are in the North-East region. However, soils affected by salts are also found in the state of Rio Grande do Sul and Pantanal of Mato Grosso (Ribeiro et al. 2009). These authors also reported that in Brazil soils affected by salts are about 160.000 km^2 or 2 % of the national territory. Major part of the soils affected by salinity are in the state of Bahia (44 % of total), followed by state of Ceará with 26 % of total area. Salinity in irrigated lands is determined by irrigation water quality, irrigation method, drainage, soil permeability, and water table. In Brazil, salinity is mostly prevailing in the dry area of nine states of the North-East. In some irrigated areas of North-East, salinity decreased yield of crops and farmers abandoned these lands. It is estimated that about 20 % of the irrigated areas of the North-East of Brazil are affected by salinity.

About 20 % of cultivated area and 33 % of irrigated area is affected by salinity worldwide and this area is mostly located in Asia (Rains and Goyal 2003, Ashraf and Foolad 2007). Worldwide about 1 billion ha of land is affected by salinity. According to Pessarakli and Szabolcs (1999), all continents have salinity problem, except Antarctica. In addition, salinity problem is increasing at a rate of 10 % annually (Szabolcs 1994). These data are alarming because world population from 7 billion people in 2011 to be expected to increase about more than 9 billion people in 2050 (Epstein and Bloom 2005). Major part of this population increase will be in the developing countries where food demand is higher. In this context, incorporation of land areas affected by salts in crop production have important role in future from social and economic point of view (Fageria et al. 2010). Furthermore, urbanization and industrialization will increase competition for fresh water (Rains and Goyal 2003). Hence, inadequate soil and water management will increase salinity problem worldwide (National Academy of Sciences 1999).

Soils affected by salts are defined as those which are adversely modified for growth and development of most crop species due to presence of soluble salts, exchangeable sodium or both in the rhizosphere (Soil Science Society of America 2008). Soluble salts normally present in salt affected soils are cations such as Ca^{2+}, Mg^{2+}, Na^{+} and anions SO_4^{2-}, Cl^{-}, HCO_3^{-}, and sometimes K^{+}, CO_3^{2-}, and NO_3^{-}. Soils affected by salts are mostly common in arid and semi-arid regions due to low precipitation and high evaporation. These climatic conditions do not permit salt lixiviation from the soil profile and accumulate in quantity toxic for plant growth. Salinity problem also occurs in areas near sea shore due to flooding by sea water which contain high salts (Fageria et al. 2010). Use of inappropriate levels of fertilizers with inadequate management practices can create saline conditions even in humid conditions (Fageria et al. 2011a).

Table 7.1 Salt affected area in the world

Region	Area in 1.000 hectares		
	Saline	Sodic	Total
North America	6,191	9,564	15,755
Mexico and Central America	1,965	–	1,965
South America	69,410	59,573	128,983
Africa	53,492	26,946	80,438
South Asia	83,312	1,798	85,110
North and Central Asia	91,621	120,065	211,686
East Asia	19,983	–	19,983
Australia and New Zealand	17,359	339,971	357,330
Total	343,333	557,917	901,250

Source Adapted from Lal et al. (1989)

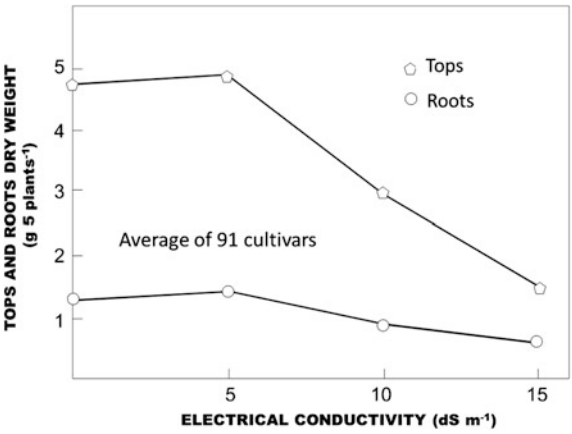

Fig. 7.1 Relationship between salinity levels and dry matter of shoots and roots of lowland rice. Adapted from Fageria (1992)

Negative effects of salinity on agriculture are a concern because it affects growth and development and yield of crop plants. Typically, decrease in growth of plants occurs linearly after attending threshold value of salinity. Leaves of salt affected plants are small and show dark green color in comparison with leaves of normal plants. Generally, salinity effects on plants do not show yellowing or discoloration such as nutritional deficiency. Salinity decreases water absorption but wilting symptoms of leaves rarely occur. Under saline conditions moderately low water potentials are always present and water potential changes are usually gradual. Plants are, therefore, hardened by the continual stress and are less apt to exhibit abrupt change in turgor. Plants also do not show symptoms such as marginal or tip burn of leaves, occur as a rule only in woody plants in which these symptoms indicate toxic accumulations of chloride or boron. Salinity decreases root growth as well as shoot growth but this reduction is lower in roots compared to tops growth (Fig. 7.1). Besides generally stunting plant growth, salinity causes many specific anatomic changes that are often related to the ionic composition of the root media. Chloride

Table 7.2 Influence of salinity on P and K contents in the tops of two irrigated rice genotypes

Salinity level (ds m^{-1} at 25 °C)	CNA 810098		CNA 810162[a]	
	P conc. (g kg^{-1})	K conc. (g kg^{-1})	P conc. (g kg^{-1})	K conc. (g kg^{-1})
0.29 (control)	2.9	35.5	2.5	34.0
5	2.7	32.5	2.0	32.8
10	2.4	25.7	2.1	24.3
15	1.5	22.5	–	–

[a] Genotype CNA 810162 did not produce dry matter at high salinity level; therefore, P and K concentrations were not determined
Source Adapted from Fageria (1985b)

salinity may cause larger epidermal cells, fewer stomata per unit leaf area, and a poorly developed xylem system. In contrast, sulfate salinity produces smaller cells and an increased number of stomata per unit leaf area.

Growth of rice plants decreases with the increase of salts in the root zone. The decrease in plant growth is related to increase in osmotic tension of soil solution which reduced absorption of water by roots due to accumulation of various ions in toxic amount (Saqib et al. 2005, 2008; Ribeiro et al. 2009). Toxic effects of sodium is highly notable effect of salinity on plant growth (Saqib et al. 2008). With the increasing concentration of Na^+ and Cl^-, concentrations of P, K^+, and Ca^{2+} reduced in the plants (Kumar et al. 2008; Fageria et al. 2011b). In the salt affected environment there is preponderance of nonessential elements over essential elements. In the salt affected soils, plants must absorb the essential nutrients from a diluted source in the presence of highly concentrated nonessential nutrients. This requires extra energy and plants sometimes unable to fulfill their nutritional requirements. There are two main stresses imposed by salinity on plant growth. One is water stress imposed by the increase in osmotic potential of the rhizosphere as a result of high salt concentration. Another stress is toxic effect of high concentration of ions. Hale and Orcutt (1987) reported that if the salt concentration is high enough to lower the water potential by 0.05–0.1 MPa then plant is under salt stress. If the salt concentration is not this high, the stress is ion stress and may be caused by one particular species of ion (Hale and Orcutt 1987).

In Table 7.2 salinity effects on absorption of P and K^+ by two rice genotypes can be observed. The concentration of two nutrients decreased with the increasing salinity level. Uptake of high amount of Na^+ and Cl^- reduced uptake of cations and anions and created nutritional disequilibrium in the plants, and reduced yield (Kumar et al. 2008; Fageria et al. 2011b). Hence, plants tolerant of salinity exclude Na^+ in absorption process and tried to maintain high concentration of K^+ in tops (Davenport et al. 2005; Saqib et al. 2005). High K^+/Na^+ ratio in plant tissue is considered a good indicator of salinity tolerance (Wei et al. 2003). High salt concentration in the root zone reduced photosynthesis of plants and increase respiration and consequently reduced growth (Khadri et al. 2006). Soil salinity is measured by concentration of salts or electrical conductivity. Effects of electrical conductivity on growth of crop species are presented in Table 7.3. The pH of

Table 7.3 Crop response to salinity influenced by electrical conductivity of saturated soil extract

Electrical conductivity (dS m^{-1} a 25 °C)	Crop response
0–2	Salinity effect is practically zero
2–4	Reduction in yield of very sensitive crops
4–8	Reduction in yield of most crops
8–16	Only tolerant crops produce satisfactory yield
>16	Few highly tolerant crops produce satisfactory

Source Adapted from Mengel et al. (2001)

saline soils is generally in the range of 7–8.5 (Mengel et al. 2001). If exchangeable sodium percentage (ESP = exchangeable Na/CEC × 100) is higher than 15 %, soils are called saline-sodic.

There are two options of reducing salinity problem. One is improving plants for adaptation to saline environment and other is improving soil conditions for good growth of plants. Second option implicates irrigation and drainage and high cost of operation. Information available in the literature indicates that beside soil recovery, use of salinity tolerant crop species or genotypes within species is a very attractive strategy for crop production in saline soils (Fageria et al. 2011b). However, a combination of these two methods may be more appropriate strategy to improve crop yields on salt affected soils.

7.2 Germplasm and Genetic Variability

Plant growth in saline soils depends on crop species, concentration of salts in the rhizosphere and environmental factors. Information about tolerance of crop species is fundamental for adequate management of salt affected soils. There is sufficient data in the literature showing relative tolerance of crop species to salinity. Data presented in Table 7.4 show salinity threshold values for different crop species, decrease in yield per unit of salinity increase beyond threshold and relative tolerance to salinity. Many crops seem to tolerate salinity equally well during seed germination and later growth stage. The salt tolerance of some crops, however, does change with growth stage. For example, barley, wheat, and corn are more sensitive to salinity during early seedling growth than during germination or later growth stages, wheat sugar beet and safflower are relatively sensitive during germination. The tolerance of soybean may either increase or decrease from germination to maturity, depending on the variety.

7.3 Stress Induction and Selection Strategy

To develop cultivars tolerant to salinity, first step is to identify genotypes tolerant to salinity. To achieve this objective evaluation of germplasm can be done under controlled conditions. The methodology for evaluation to salinity or other abiotic

Table 7.4 Salinity threshold, decrease in yield, and crop tolerance to salinity

Crop	Electrical conductivity of saturated soil extract		Classification[a]
	Threshold (dS m^{-1})	Yield decrease (% per dS m^{-1}above threshold)	
Fiber, grain, and special crops			
Cotton	7.7	5.2	T
Peanut	3.2	29.0	MS
Rice	3.0	12.0	S
Oats	–	–	MT
Sugar beet	7.0	5.9	T
Sugarcane	1.7	5.9	MS
Cowpea	4.9	12.0	MT
Rye	–	–	MT
Barley	8.0	5.0	T
Dry bean	1.0	19.0	S
Sunflower	–	–	MS
Guar	–	–	MT
Flax	1.7	12.0	MS
Millet	–	–	MS
Corn	1.7	12.0	MS
Soybean	5.0	20.0	MT
Sorghum	6.8	16.0	MT
Wheat	6.0	7.1	MT
Triticale	–	–	T
Grasses and forages			
Alfalfa	2.0	7.3	MS
Bermuda grass	6.9	6.4	T
Sudan grass	2.8	4.3	MT
Tall fescue	3.9	5.3	MT
Sesbania	2.3	7.0	MS
Ladino clover	1.5	12.0	MS
Red clover	1.5	12.0	MS
Vegetable and fruit crops			
Lettuce	1.3	13.0	MS
Asparagus	4.1	2.0	T
Potato	1.7	12.0	MS
Sweet potato	1.5	11.0	MS
Eggplant	–	–	MS
Broccoli	2.8	9.2	MS
Onion	1.2	16.0	S
Carrot	1.0	14.0	S
Cauliflower	–	–	MS
Pea	–	–	S
Spinach	2.0	7.6	MS
Watermelon	–	–	MS
Strawberry	1.0	33.0	S
Radish	0.9	9.0	MS

(continued)

Table 7.4 (continued)

Crop	Electrical conductivity of saturated soil extract		Classification[a]
	Threshold (dS m^{-1})	Yield decrease (% per dS m^{-1}above threshold)	
Cucumber	2.5	13.0	MS
Turnip	1.2	13.0	MS
Cabbage	1.8	9.7	MS
Tomato	2.5	9.9	MS

[a] *S* Sensitive, *MS* moderately sensitive, *T* tolerant, *MT* moderately tolerant
Source Adapted from Maas (1986)

Table 7.5 Nutrient solution composition for seed germination

Reagents	Nutrient	Concentration	
		mg L^{-1}	M × 10^{-4}
NH_4NO_3	N	40.00	28.170
NaH_2PO_4	P	4.00	1.290
K_2SO_4	K	40.00	10.230
$CaCl_2$	Ca	40.00	10.000
$MgSO_4.7H_2O$	Mg	40.00	16.450
$(NH_4)_6MO_7O_{24}.4H_2O$	Mo	0.05	0.005
$MnCl_2.4H_2O$	Mn	0.50	0.090
H_3BO_3	B	0.20	0.185
$ZnSO_4.7H_2O$	Zn	0.01	0.001
$CuSO_4.5H_2O$	Cu	0.01	0.001
Fe-EDTA	Fe	0.50	0.089

stress should be simple, economic, and easily adopted. Fageria (1985a) developed a technique to evaluate rice genotypes for salinity tolerance. An important component of this methodology is germinating the seeds of genotypes in solution culture. To obtained good germination, seeds should be treated with 0.1 % solution of $HgCl_2$ for 10 min and followed a washing with distilled water and put on nylon screen floating in nutrient solution. Each genotype should be germinated in a plastic pot having capacity of about two liters. Germinating pots should be covered with another bigger pot having black color or painted with black color. Composition of nutrient solution utilized in this technique is given in Table 7.5. After germination, pots covered germinating pots should be removed and seedlings should be left in the nutrient solution for about a week (Fig. 7.2). Seedlings of 7–10 days old can be transplanted in plastic tray having dimension of 30 × 45 × 8 cm with determined salinity level (Fig. 7.3). To create salinity level, 5 kg soil should be put in each tray and this soil should be mixed with a 0.5 % NaCl solution of 4 liter 3 days before transplanting. Each tray should also receive 1 g ammonium sulfate, 1.8 g triple superphosphate, 1 g potassium chloride, and 0.25 g zinc sulfate as basal fertilizer application. Twelve seedlings of each genotype should be planted in each tray. After seedling

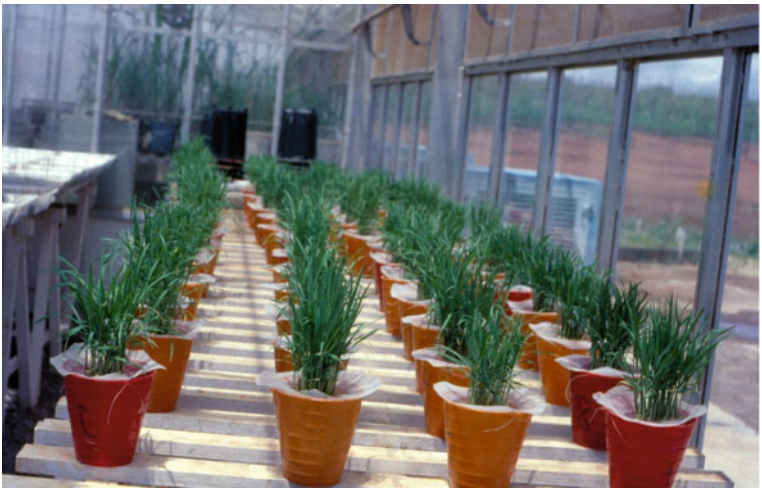

Fig. 7.2 Growth of rice seedlings in nutrient solution

Fig. 7.3 Growth of rice cultivars at low and high salinity levels

transplanting, soil in the tray should be flooded with distilled water to a depth of about 1 cm. Four weeks after transplanting percentage of dead leaves in each tray should be counted (Table 7.6) and cultivars/genotypes should be classified for salinity tolerance. Score to classify cultivars to salinity is given in Table 7.7.

Tops dry weight can also be used as a criterion to classify cultivars tolerant to salinity. In this case, minimum two levels of salinity should be imposed. One is control and another level which can affect plant growth significantly. Equation to

Table 7.6 Classification of rice cultivars tolerance to salinity based on dead leaves

Dead leaves (%)	Score	Classification
0–20	1	Tolerant
21–35	2	Tolerant
36–50	3	Tolerant
51–70	5	Moderately tolerant
71–90	7	Moderately sensitive
91–100	9	Sensitive

Source Adapted from Ponnamperuma (1977)

Table 7.7 Classification of rice genotypes to salinity tolerance

Genotype	Dead leaves (%)	Score	Classification[a]
IR 5624-164-2-1	20	1	T
IR 9129-102-2	12	1	T
BG 11-11	18	1	T
IR 4422-164-3-6	34	2	T
IR 4432-28-5	35	2	T
Tox 711-22	35	2	T
Takatiya	38	3	T
IR22	47	3	T
IR 841-63-51-9-33	41	3	T
IR 3511-39-3-3	53	5	MT
Tox 711-16	55	5	MT
Suvale1	59	5	MT
BG 90-1	64	5	MT
De Abril	71	7	MS
IR2153-43-2-5-4	71	7	MS
Tox 711-11	71	7	MS
Labelle	77	7	MS
Paga Dívida	88	7	MS
IRGA 408	90	7	MS
IAC 435	91	9	S
BR 4	91	9	S
IAC 120	95	9	S
IR26	100	9	S
IR 8	100	9	S
EEA 405	100	9	S

[a] *T* Tolerant, *MT* moderately tolerant, *MS* moderately sensitive, *S* Sensitive
Source Fageria et al. (1981)

determine reduction of dry matter with the addition of salinity treatment and interpretation of salinity tolerance results are presented in Table 7.8. Results obtained by this criterion about rice genotypes are given in Table 7.9. Besides this criterion, dry matter or grain yield production efficiency index can also be used to classify cultivars tolerance to salinity (Fageria 1991):

Table 7.8 Classification of crop genotypes to salinity based on dry matter and grain yield reduction

Reduction in yield (%)	Classification
0–20	Tolerant
21–40	Moderately tolerant
41–60	Moderately sensitive
>60	Sensitive

$$\text{Yield reduction} = \frac{\text{Yield without salinity} - \text{Yield with salinity Yield without salinity}}{} \times 100$$

Source Fageria (1985a)

Table 7.9 Influence of salinity on dry matter yield of tops (g/5 plants) of rice genotypes and their classification for salinity tolerance

Genotype	Electrical conductivity (dS m^{-1})			Reduction in dry matter yield (%)	
	Control (0,29)	5	10	5	10
CNA 810098	3.30	3.25	2.76	2 (T)	16 (T)
CNA 810112	3.76	2.85	0.97	24 (MT)	74 (S)
CNA 810115	4.66	3.33	1.67	29 (MT)	64 (S)
CNA 810129	2.99	2.89	1.13	3 (T)	62 (S)
CNA 810138	3.76	2.16	1.37	43 (MS)	64 (S)
CNA 810168	3.12	2.69	1.96	14 (T)	38 (MT)

T tolerant, *MT* moderately tolerant, *MS* moderately sensitive, *S* sensitive
Source Fageria (1985b, 1992)

$$\text{DM or GY efficiency index} = \frac{Y_1}{AY_1} x \frac{Y_2}{AY_2}$$

Where DM = dry matter, GY = grain yield, Y_1 = dry matter or grain yield at low salinity level, AY_1 = average dry matter or grain yield of genotypes at low salinity level, Y_2 = dry matter or grain yield at high salinity level, and AY_2 = average dry matter or grain yield of genotypes at high salinity level. When DM or GY efficiency index is higher than 1.0, cultivars should be classified as tolerant, DM or GY efficiency index in the range of 0.5–1.0, cultivars should be classified as moderately tolerant and when this index is lower than 0.5, cultivars should be classified as sensitive to salinity (Table 7.10).

7.4 Heridity, Parents Effect and Relationship Among Traits

Understanding genetic base to salinity tolerance of crop species is very important because breeding procedure for this stress depend on heredity pattern, quantitative and qualitative number of genes with major effect, and nature of their action

Table 7.10 Influence of salinity on tops dry weight of rice (g) and their classification for salinity tolerance based on yield efficiency index (YEI)

Cultivar/Lines	Salinity level (dS m^{-1})		YEI and classification[a]
	Control (0.29)	10	
GA 3459	1.16	0.42	0.60 (MT)
L 440	1.99	0.47	1.16 (T)
IET 2881	1.87	0.81	1.88 (T)
GA 3461	1.32	0.49	0.80 (MT)
CNA 12	1.92	0.56	1.33 (T)
GA 3452	1.96	0.59	1.53 (T)
CNA 294-B-BM-4-4	1.85	0.61	1.40 (T)
CNA 237-F-130-1	1.57	0.56	1.09 (T)
CNA 108-B-28-2-1	1.15	0.16	0.23 (S)
CNA 296-B-BM-M-4	1.63	0.28	0.56 (MT)
Average	1.64	0.49	

[a] *T* tolerant, *MT* moderately tolerant, *MS* moderately sensitive, *S* sensitive
Source Fageria (1985a)

(Rao and McNeilly 1999). In rice spikelet sterility which is important trait affecting yield under saline conditions at least by three genes. Diallel analysis showed effect of salinity on seedlings and spikelet sterility suggested additive as dominant and some of high heritability (Flowers 2004). There is also evidence of dominancy of salinity tolerance in sorghum. Diallel analysis, based on NaCl tolerance, expressed as root length of salt treated plant compared without salt treated plant, showed that there was an additive effect and dominant by NaCl. In corn Rao and McNeilly (1999) reported that salinity tolerance in the vegetative growth stage was governed by genes having additive effect and not the non additive. Exploiting heterosis can be helpful in finding material for salinity tolerance. Virmani (2003) reported that heterosis pattern in hybrid rice was significant in saline soil compared with normal soil condition in Egypt. In Philippines, hybrid rice presented higher tolerance to salinity compared to inbreed lines. These examples prove that salinity tolerance is genetically complex, presenting heterosis, dominant, and additive effects (Flowers 2004).

7.5 Breeding Methods

Developing crop plants tolerant to salinity is very important strategy to improve yield on salt affected soils. Ashraf et al. (2008) reported that salinity tolerance is very complex matter at both the whole plant level and the cellular level, involving interaction of stress with molecular, biochemical, and physiological processes at different stages of plant growth and development. The genetic variation to salinity is very low for most crop species which makes difficult breeding for this stress by conventional techniques. Chinnusamy et al. (2005) reported that conventional

Table 7.11 Cultivars of some crop species commercially released for cultivation

Cultivar (species)	Selection method	Country (year of release)
Arsola 1–18 (avocado)	Cultivar crossing	USA (1951)
Nebraska 10 (agropyron)	Natural selection of ecotype	USA (1962)
AZ Germ Salt 1 (alfalfa)	Back crossing selection	USA (1983)
Arizona 8601 (corn)	Natural selection program	USA (1987)
AZ Germ Salt 2 (alfalfa)	Back crossing selection	USA (1990)
Giza 159 (rice)	Cultivar crossing	Egypt (1966)
Edkway (tomato)	Natural selection program	Egypt (1982)
Giza 160 (rice)	Cultivar crossing	Egypt (1984)
Saltol (red fescue)	Natural selection of ecotype	Canada (1981)
BG 84-3 (melon)	Natural selection of ecotype	Israel (1990)

Source Adapted from Shannon (1996) and Noble and Rogers (1992)

breeding for salt tolerance is very time consuming, undesirable genes are often transferred along with desirable traits and reproductive barriers restrict transfer of favorable alleles from interspecific and intergeneric sources. However, there has been progress in developing crop cultivars tolerant to salinity by conventional breeding (Ashraf 1994). Data in Table 7.11 show commercially released cultivars of some crop species to salinity tolerance. Utilizing wild relatives of crop plants as a source of genes conferring salt tolerance can broaden the range of variation that can be used in crop production. However, Ashraf et al. (2008) reported that incorporating tolerance genes from wild relatives into domesticated crops is difficult because of reproductive barriers and there are very few examples of effectiveness of this approach in the literature.

7.6 Use of Biotechnology for Breeding to Salinity Tolerance

Conventional breeding had contributed to developing crop cultivars for salinity tolerance. However, the progress so far has not been significant. Hence, modern techniques like soma-clonal variation, protoplasmic fusion, and mutation breeding can contribute significantly in breeding crop cultivars for salinity tolerance, if the traits for salt tolerance do not exist or if the genetic variability for specific traits is absent (Ashraf 1994). The prime strategy in mutation based breeding is to induce or alter one or two major traits through mutagens, which may be chemical or radiation (Ashraf et al. 2008). There has been experimental evidence that rice mutants NIAB Rice- 1 and PSR 1–84 have shown greater yield than their respective salt-tolerant check cultivars, Pokkali and Johna 349, under saline conditions (NIAB 1987). In addition, the use of chemical mutagens in developing salt-tolerant rice mutants has also been shown to be successful. Ashraf (1984) induced variability for salt tolerance in the salt sensitive rice cultivar Taichung 65 by treating fertilizer egg cells with varying doses of N-methyl-N-nitrosourea.

In M_3, two salt-tolerant mutants were detected that had 83 % and 90 % survival at the seedling stage in 0.5 % NaCl.

Genetic markers (RAPD, AFLP, and SSR) that have been routinely used in fingerprints, genetic mapping, and quantitative trait loci (QLT) analysis may help in identifying useful mutations (Mlcochová et al. 2004) induced by chemical mutagens or radiations and may help in examining its physiological bases, which will bring a new dimension in gene technology. Molecular biology can also play a significant role in incorporating salt resistant genes in crop plants. Advance in molecular biology leads to development of molecular marker of DNA which can be used to identify QTLs. Over the last two decades, advances in molecular marker technology have led to the development of detailed molecular linkage maps for many plant species. The DNA based markers speed up the advance in improvement of crops for stress tolerance (Vinh and Paterson 2005). Furthermore, DNA markers can be used as a diagnostic tool to identify genotypes in large populations that bring together superior genetic potential for productivity under stress, with the traits that are necessary to develop a potential commercial cultivar (Vinh and Paterson 2005; Ashraf et al. 2008).

The effectiveness of QTL mapping in transferring stress genes is very high. It is reported that QTL mapping is a way to estimate the locations, numbers, extent of phenotypic effects and modes of gene action, and of individual determinants that substantially contribute to the inheritance of continuously variable traits (Vinh and Paterson 2005). The principal objective is to isolate genetic signals emerging from an individual locus, the background collective effects of nongenetic factors, as well as measurement errors in evaluation of continuous traits. The QTL mapping is thus an effective means for identifying specific components that allow direct assessment of stress tolerance (Ashraf et al. 2008). The QTLs and marker-assisted selection offer several advantages over direct phenotypic screening, in as much as the PCR-based techniques used to identify the markers reduce the time needed to screen genotypes as well as reduce the environmental impact on the trait under study.

There are several reports in the literature that genetic engineering is an important tool in gene transfer across reproductive barriers. In addition, genetic engineering offers a way to create new genetic variation when natural allelic variation may be limited or inappropriate (Humphreys and Humphreys 2005). Yamaguchi and Blumwald (2005) reported that there are two genetic approaches which are currently being used to improve crop stress tolerance These approaches are: (1) utilization of natural genetic variation, either through direct selection in stressful conditions or through the mapping of QTLs and subsequent marker-assisted selection, and (2) production of transgenic plants by introducing the novel genes or by modifying the expression of the existing genes to alter degree of stress tolerance. Large-scale screening of crop genotypes for salinity tolerance can be done by dissection of complex salt tolerance trait by means of QTL mapping and identifying chromosomal regions associated with DNA markers (Ashraf et al. 2008).

7.7 Transgenic Method

Ashraf et al. (2008) defined transgenic crops are bioengineered crops that possess a gene or genes that have been inserted by human into their genome using modern biotechnology. These authors further said that the inserted gene sequence, known as the transgene, may belong to an unrelated plant, or even to a bacterium or animal. Crops that contain these transgene are also described as genetically modified and are often referred to as genetically modified plants (Ashraf et al. 2008). Transgenic approach is widely used by plant scientists to develop crop cultivars to biotic and abiotic stresses. Advances in molecular biology have led the identification of a large number of genes that are induced as a result of drought or salinity stress (Lea et al. 2004). The major focus of research suing transgenic method or approach are genes that encode: (i) compatible osmotic (GB, proline, sugars) (ii) transcription factors (iii) enzymatic and nonenzymatic antioxidants (iv) ion transport proteins, and (v) heat shock and late embryogenesis abundant (LEA) proteins (Ashraf et al. 2008).

In transgenic rice plants, overexpressing peroxisomal BADH exhibited enhanced ion selectivity under saline conditions by accumulating high amounts of K^+ but low amounts of Na^+ and Cl^- (Kishitani et al. 2000). However, it is not yet clear how GB overproduction increases the K^+/Na^+ ratio, which is regulated by ion transporters and channels (Ashraf et al. 2008). In general, proline accumulation in response to abiotic stresses including salt stress is found to be correlated with stress tolerance of many plants (Ashraf and Harris 2004). Zhu et al. (1998) reported that genetically modified rice plants showed faster recovery after a short period of salt stress compared to inbred rice plants.

Although genetic engineering plants to overproduce proline or GB seems to be an effective means of increasing salinity tolerance, some failures of this approach are also reported in the literature (Ashraf and Foolad 2007). It is also apparent that salt tolerance in plants depends on both the level of accumulation of compatible solutes and their subsequent transportation to target compartments (Chinnusamy et al. 2005). For example, transgenic plants expressing choline oxidase targeted to chloroplasts exhibited higher resistance to photoinhibition under salt and cold stresses than did transgenic plants with choline oxidase targeted to the cytosol (Sakamoto et al. 1998). Considering various strategy available to induce salt tolerance in plants, it is suggested that all factors associated with gene regulation at transcriptional and translational levels should be examined while engineering plants for these compatible solutes (Ashraf et al. 2008).

Ashraf et al. (2008) and Garg et al. (2002) reported that transgenic rice expressing the trehalose gene is responsible for multi stress tolerance such as salinity, drought, and cold stress. Similarly, transgenic rice plants expressing chimeric gene Ubi1::TPSP accumulated a high levels of trehalose that resulted in increased tolerance of drought, salt, and cold, as shown by chlorophyll florescence and growth inhibition analyses (Jang et al. 2003). However, several pleiotropic effects observed in these transgenic led to the suggestion that trehalose affects other plant development process as well (Ashraf et al. 2008).

Sugar alcohols, such as glycerol, mannitol, sorbitol, and D-ononitol, are potential osmoprotectants in many halophytes (Yancey et al. 1982). Transgenic tobacco and wheat plants expressing the *mt1D* gene, responsible for the biosynthesis of mannitol, were found to be tolerant to salt stress (Tarczynski et al. 1993, Abebe et al. 2003).

Ectoine is another important compatible solute and is generally accumulated in halophytic bacteria. Its introduction into plants can also alleviate adverse effects of salt stress. Tobacco plants transformed with three genes isolated from halophytic bacteria *Halomas elongata*, which are responsible for biosynthesis of ectoine, when treated with NaCl accumulated more ectoine and showed greater growth than untransformed plants (Moghaieb et al. 2006).

Plants can produce various antioxidants and detoxifying enzymes to efficiently scavenge reactive oxygen species (ROS), that can cause considerable oxidative damage to membrane lipids, proteins, and nucleic acids. The various antioxidants used by plants are ascorbate, glutathione, α-tocopherol, and carotenoids, whereas detoxifying enzymes include superoxide dismutase (SOD), catalase, peroxidase, and enzymes of ascorbate–glutathione cycle. However, it is crucial to target enzymes at the site where the stress-induced ROS production takes place for detoxification and hence improved stress tolerance. This indicates that proteins that are damage by oxidative stress have a significant adverse effect on plant tolerance to environmental stresses. Tobacco plants modified to overexpress glutathione S-transferase/glutathione peroxidase, one of the major enzymes of ascorbate–glutathione cycle, were found to be tolerant to both chilling and salt stresses (Roxas et al. 1997, 2000).

Most oxidative stress is triggered by methionine oxidation resulting in disruption of protein structure (Hoshi and Heinemann 2001). Oxidized methionine can be reduced back to methionine by the activity the enzyme methionine sulfoxide reductase (MSR) (Sadanandom et al. 1996). Romero et al. (2004) demonstrated that plant lines overexpressing MSR4 in chloroplasts have increased resistance to oxidative damage and are expected to be salt tolerant because higher antioxidant capacity of a plant is associated with salt tolerance (Gossett et al. 1996).

Some aldehyde dehydrogenases are known to have a role in osmoregulation by catalyzing the synthesis of osmoprotectants (Kirch et al. 2004). Rodrigues et al. (2006) showed that both tobacco and *Arabidopsis* expressing aldehyde dehydrogenase *GmALDH7* showed greater germination and reduced reactive aldehydes, which are generated by lipid peroxidation, under saline conditions. These findings indicate that *GmALDH7* is one of the most effective genes for producing salt-stress-tolerant plants.

Aharon et al. (2003) found that overexpression of the vacuolar Na^+/H^+ antiporter that sequesters Na^+ in vacuoles (NHX1) improved the salinity tolerance in *Arabidopsis*, tomato, and *Brassicas*. Ohta et al. (2002) and Fukuda et al. (2004) found that the salt tolerance of transgenic rice overexpressing halophyte (*Atriplex gmelini*) gene *AgNHX1* and rice gene *OsNHX1* was improved compared with wild types. However, the increase of leaf Na^+ was similar in both the transgenic and wild-type plants. These results indicate that the Na^+/H^+ antiporter gene could

sequester part of the Na^+ in the vacuoles and prevent the toxic effects of excessive Na^+ ions on the cells.

Active transport of Na^+ across plant cell membranes is usually coupled to the proton (H^+) electrochemical potential established by H^+-translocating pumps (Gaxiola et al. 2001). From this finding, it is suggested that overexpression of cation transporters in combination with H^+-translocating pumps can increase salt tolerance. Zhao et al. (2006) reported that the coexpression of *Suaeda salsala SsNHX1* and *Arabidopsis AVP1* in transgenic rice caused greater improvement in salt tolerance than transformation with the single gene, *SsNHX1*.

During the last two decades, many abiotic stress-inducible genes have been cloned and characterized from different plant species. However, for the expression of these genes, there is a need to identify suitable promoters. Efforts have been made to identify and characterize stress-induced promoters, particularly those induced by anaerobic conditions, low or high temperatures or salt stress (Grover et al. 2001). For example, the production of transgenic plants with *DREB* genes is useful for improvement of tolerance of environmental stresses in a number of species. However, constitutive expression of these genes retards plant growth. Development of transgenic plants with stress-inducible promoters along with *DREB* genes or regulation of expression of *DREB* genes by stress-inducible promoters can induce stress tolerance and minimize the adverse effects of stress on growth. For the effective application of molecular approaches to producing stress-tolerant plants, it would be desirable to restrict transgene expression to particular tissues by the use of tissue-specific promoters (Gittins et al. 2001).

Several groups of late embryogenesis abundant (LEA) protein genes have been demonstrated to confer water deficit and salt-stress tolerance. Expression of *HVA1*, a group 3 LEA protein from barley, conferred tolerance to soil water deficit and salt stress in transgenic rice plants (Babu et al. 2004).

Although transgenic approaches for enhance abiotic stress tolerance are gaining ground among both scientists and public, the achievements made so far are not significant. This has been due to the fact that scientists have been producing transgenic of various crops in the past using single-gene transfer that undoubtedly resulted in transgenics with limited stress tolerance. However, there is a growing trend now to use the multigene approach by which several genes responsible for overall stress tolerance are simultaneously transferred to the transgenics (Cherian et al. 2006). Furthermore, other protocols such as RNAi and transposon insertional knockouts for the candidate stress-tolerant genes and signaling pathways show a great promise to produce highly stress-tolerant crop plants.

7.8 Conclusions

Salinity is a serious problem in worldwide including Brazil. Salt affected soils can be defined as those soils that have been adversely modified for the growth of most crop plants by the presence of soluble salts, with or without high amounts of

exchangeable sodium. Civilizations have been destroyed by the encroachment of salinity on the soils, as a result of vast areas of the land is rendered unfit for agriculture. Salt affected soils are found in many regions of the world. Salt affected soils normally occur in arid and semi-arid regions where rainfall is insufficient to leach salts from the root zone. Salt problems, however, are not restricted to arid or semi-arid regions. They can develop even in sub-humid and humid regions under appropriate conditions. In addition, these soils may also occur in coastal areas subject to tides. Salts generally originate from native soil and irrigation water. Roughly 263 million hectares are irrigated area worldwide and in most of that area salinity is a growing threat. The irrigated area represents about 20 % of the total land used for crop production. This represents about 19 % of the total area of the world under crop production. Use of inappropriate levels of fertilizers with inadequate management practices can create saline conditions even in humid conditions. Salinization is the process whereby soluble salts accumulate in the root zone. Common ions contributing to this problem are Ca^{2+}, Mg^{2+}, Cl^{-}, Na^{+}, SO_4^{2-}, HCO_3^{-} and in some cases K^{+} and NO_3^{-}. Salinity can be measured by determining electrical conductivity of the saturated soil extract.

The important soils and plant management practices which can improve crop yield on salt affected soils are use of soil amendments to reduce effect of salts, application of farmyard manures to create favorable plant growth environments, leaching salts from soil profile, and planting salt-tolerant crop species or genotypes within species. Addition of fertilizers, especially potassium may also help in reducing salinity effects and improving nutrient use efficiency. Breeding salt tolerance cultivars by conventional methods has limited success due to several reasons. Hence, genetic engineering seems to offer considerable promise for the development of salinity tolerant plants, including cultivars of important food crops.

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